

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/576,424

DATE: 11/02/2001

TIME: 12:15:58

Input Set : A:\37275681.app

Output Set: N:\CRF3\11022001\I576424.raw

3 <110> APPLICANT: ANDERSON, DARRELL R.
 4 HANNA, NABIL
 5 BRAMS, PETER
 6 HEARD, CHERYL
 8 <120> TITLE OF INVENTION: INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
 9 CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
 10 CO-STIMULATORY ANTIGENS
 12 <130> FILE REFERENCE: 37003-275681
 14 <140> CURRENT APPLICATION NUMBER: 09/576,424
 15 <141> CURRENT FILING DATE: 2000-05-22
 17 <150> PRIOR APPLICATION NUMBER: PCT/US97/19906
 18 <151> PRIOR FILING DATE: 1997-10-29
 20 <150> PRIOR APPLICATION NUMBER: 08/746,361
 21 <151> PRIOR FILING DATE: 1996-11-08
 23 <150> PRIOR APPLICATION NUMBER: 08/487,550
 24 <151> PRIOR FILING DATE: 1995-06-07
 26 <160> NUMBER OF SEQ ID NOS: 12
 28 <170> SOFTWARE: PatentIn Ver. 2.1
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 705
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (1)..(702)
 39 <400> SEQUENCE: 1
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 42 1 5 10 15
 44 ggt gca cga tgt gcc tat gaa ctg act cag cca ccc tcg gtg tca gtg 96
 45 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
 46 20 25 30
 48 tcc cca gga cag acg gcc agg atc acc tgt ggg gga gac aac agt aga 144
 49 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
 50 35 40 45
 52 aat gaa tat gtc cac tgg tac cag cag aag cca gcg cgg gcc cct ata 192
 53 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
 54 50 55 60
 56 ctg gtc atc tat gat gat agt gac cgg ccc tca ggg atc cct gag cga 240
 57 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
 58 65 70 75 80
 60 ttc tct ggc tcc aaa tca ggg aac acc gcc acc ctg acc atc aac ggg 288
 61 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
 62 85 90 95
 64 gtc gag gcc ggg gat gag gct gac tat tac tgt cag gtg tgg gac agg 336
 65 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
 66 100 105 110

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68 gct agt gat cat ccg gtc ttc gga gga ggg acc cgg gtg acc gtc cta 384
69 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
70      115      120      125
72 ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct 432
73 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
74      130      135      140
76 gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac 480
77 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
78 145      150      155      160
80 ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc 528
81 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
82      165      170      175
84 gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac 576
85 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
86      180      185      190
88 aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag 624
89 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
90      195      200      205
92 tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg 672
93 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
94      210      215      220
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97 Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
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111      20      25      30
113 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
114      35      40      45
116 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
117      50      55      60
119 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
120 65      70      75      80
122 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
123      85      90      95
125 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
126      100      105      110
128 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
129      115      120      125
131 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
132      130      135      140
134 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
135 145      150      155      160

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137 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
138                               165                               170                               175
140 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
141                               180                               185                               190
143 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
144                               195                               200                               205
146 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
147       210                               215                               220
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150 225                               230
153 <210> SEQ ID NO: 3
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156 <213> ORGANISM: Homo sapiens
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159 <221> NAME/KEY: CDS
160 <222> LOCATION: (1)..(1428)
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165   1           5           10           15
167 gtc ctg tcc cag gtg aag ctg cag cag tgg ggc gaa gga ctt ctg cag      96
168 Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
169           20           25           30
171 cct tcg gag acc ctg tcc cgc acc tgc gtt gtc tct ggt ggc tcc atc     144
172 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
173           35           40           45
175 agc ggt tac tac tac tgg acc tgg atc cgc cag acc cca ggg agg gga     192
176 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
177   50           55           60
179 ctg gag tgg att ggc cat att tat ggt aat ggt gcg acc acc aac tac     240
180 Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
181  65           70           75           80
183 aat ccc tcc ctc aag agt cga gtc acc att tca aaa gac acg tcc aag     288
184 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
185           85           90           95
187 aac cag ttc ttc ctg aac ttg aat tct gtg acc gac gcg gac acg gcc     336
188 Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
189           100          105          110
191 gtc tat tac tgt gcg aga ggc cct cgc cct gat tgc aca acc att tgt     384
192 Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
193           115          120          125
195 tat ggc ggc tgg gtc gat gtc tgg ggc ccg gga gac ctg gtc acc gtc     432
196 Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
197   130          135          140
199 tcc tca gct agc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc     480
200 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
201 145          150          155          160
203 tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag     528

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204	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
205					165					170					175		
207	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tgc	tgg	aac	tca	ggc	gcc	ctg	576
208	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
209				180					185					190			
211	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	624
212	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
213				195					200					205			
215	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	672
216	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
217		210						215						220			
219	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	720
220	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
221	225					230					235					240	
223	gac	aag	aaa	gca	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	768
224	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
225					245					250					255		
227	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	816
228	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
229				260					265					270			
231	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	864
232	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
233			275					280						285			
235	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	912
236	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
237		290					295					300					
239	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	960
240	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
241	305					310				315						320	
243	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	1008
244	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
245					325					330					335		
247	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	1056
248	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
249				340					345					350			
251	tcc	aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	1104
252	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
253			355					360						365			
255	aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	1152
256	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
257		370						375				380					
259	gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	1200
260	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
261	385					390				395						400	
263	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	1248
264	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
265					405					410					415		
267	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	1296
268	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	

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269          420          425          430
271 ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1344
272 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
273          435          440          445
275 ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1392
276 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
277          450          455          460
279 tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1431
280 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
281 465          470          475
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289 <400> SEQUENCE: 4
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294 20 25 30
296 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
297 35 40 45
299 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
300 50 55 60
302 Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
303 65 70 75 80
305 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
306 85 90 95
308 Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
309 100 105 110
311 Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
312 115 120 125
314 Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
315 130 135 140
317 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
318 145 150 155 160
320 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
321 165 170 175
323 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
324 180 185 190
326 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
327 195 200 205
329 Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
330 210 215 220
332 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
333 225 230 235 240
335 Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
336 245 250 255
338 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
339 260 265 270

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VERIFICATION SUMMARY

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